

STIC-Biotech/ChemLib

169454

From: Chernyshev, Olga
Sent: Tuesday, October 25, 2005 10:14 AM
To: STIC-Biotech/ChemLib
Subject: 10/088,724 sequence search request

Please search SEQ ID NO: 63 in regular databases.
Thank you very much!

Olga N. Chernyshev, Ph.D.
AU 1649
REM 3C89
2-0870
mail 4C70

RECEIVED

OCT 25 2005

REMOVEMENT DIVISION
(STIC)

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA#: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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OM protein - protein search, using sw model

Run on: October 26, 2005, 04:41:36 ; Search time 163 Seconds
 (without alignments)
 25.614 Million cell updates/sec

Title: US-10-088-724C-63

Perfect score: 29

Sequence: 1 PXXXXLTXXP 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 1862994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications AA: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query Match	Length	DB	ID	Description
1	22	75.9	83	16	US-10-437-963-153122	Sequence 153122,
2	22	75.9	103	16	US-10-437-11571742	Sequence 237142,
3	22	75.9	122	15	US-10-424-598-236119	Sequence 236119,
4	22	75.9	127	16	US-10-767-705-44795	Sequence 44795, A
5	22	75.9	154	16	US-10-856-498-775	Sequence 775, APP
6	22	75.9	215	15	US-10-108-260-3211	Sequence 3211, APP
7	22	75.9	286	16	US-10-856-499-920	Sequence 920, APP
8	22	75.9	306	16	US-10-437-963-172644	Sequence 172644, A
9	22	75.9	351	20	US-11-097-143-38586	Sequence 38586, A
10	22	75.9	381	14	US-10-128-714-8245	Sequence 3245, APP
11	22	75.9	390	16	US-10-437-963-139856	Sequence 139856,

RESULT 1
 US-10-437-963-153122
 Publication No. US0040123343A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovalic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 APPLICANT: Wu, Wei
 APPLICANT: Boukharov, Andrey A.
 APPLICANT: Li, Ping
 APPLICANT: Barbakow, Brad
 APPLICANT: Ili, Ping
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Title of Invention: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 3B-21(33221B
 CURRENT APPLICATION NUMBER: US/10/437,963
 CURRENT FILING DATE: 2003-05-14
 NUMBER OF SEQ ID NOS: 204966
 SEQ ID NO 153122
 LENGTH: 83
 TYPE: PRY
 ORGANISM: Oryza sativa
 FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT4530_53105C.1.pep
 US-10-437-963-153122
 Query Match 75.9%; Score 22; DB 16; Length 83;
 Best Local Similarity 40.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OQ 1 PXXXXLTXXP 10
 Db 55 PSSAELTSAAP 64

RESULT 2
US-10-425-115-237142
; Sequence 237142, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 237142
; LENGTH: 103
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 237142
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_147860C.1.pep
US-10-425-115-237142
; Query Match Similarity 75.9%; Score 22; DB 16; Length 103;
; Best Local Similarity 40.0%; Pred. No. 2.4e+02;
; Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 PXXXXLTXXP 10
Db 76 PAETSLTSP 85

RESULT 3
US-10-424-599-236119
; Sequence 236119, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 236119
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(122)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_55243C.1.pep
US-10-424-599-236119

Query Match Similarity 75.9%; Score 22; DB 15; Length 122;
Best Local Similarity 40.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 PXXXXLTXXP 10
Db 76 PSAGALTTTP 35

RESULT 4
US-10-767-701-44795
; Sequence 44795, Application US/10767701

RESULT 5
US-10-856-499-775
; Sequence 775, Application US/10856499
; Publication No. US20040259145A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C2
; CURRENT APPLICATION NUMBER: US/10/856,499
; CURRENT FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 2370
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 775
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-856-499-775

Query Match Similarity 75.9%; Score 22; DB 16; Length 154;
Best Local Similarity 40.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 PXXXXLTXXP 10
Db 140 PSSSILTESP 149

RESULT 6
US-10-108-260A-3211
; Sequence 3211, Application US/0108260A
; Publication No. US2004005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US2004005560A1, full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3211
; LENGTH: 215

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OM protein - protein search, using bw model

Run on: October 26, 2005, 04:38:06 ; Search time 41 Seconds
(without alignments)
18.207 Million cell updates/sec

Title: US-10-088-724C-63
Perfect score: 29
Sequence: 1 PXXXXLTXXP 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

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6: /cgn2_6/ptodata/1/iaa/backTries1.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Match Length	DB ID	Description
1	22	75.9	128	US-09-248-796A-22571
2	22	75.9	154	US-09-640-211A-775
3	22	75.9	286	US-09-252-991A-26404
4	22	75.9	286	US-09-640-211A-920
5	21	72.4	36	US-08-460-617-2
6	21	72.4	53	PCT-US96-08730-1
7	21	72.4	36	PCT-US96-08730-2
8	21	72.4	37	US-08-460-617-3
9	21	72.4	37	US-08-460-617-4
10	21	72.4	37	PCT-US96-08730-15
11	21	72.4	38	US-02-428-498-1
12	21	72.4	53	US-02-513-999C-6581
13	21	72.4	1334	US-02-644-460-33
14	21	72.4	148	US-02-511-999C-5275
15	21	72.4	174	US-02-252-991A-26812
16	21	72.4	387	US-02-516-1-6
17	21	72.4	387	US-10-211-412B-6
18	21	72.4	388	US-02-894-772-2
19	21	72.4	388	US-02-207-844-2
20	21	72.4	469	US-02-134-999C-5065
21	21	72.4	483	US-02-916-109-4
22	21	72.4	483	US-10-211-412B-4
23	21	72.4	483	US-02-538-092-1162
24	21	72.4	508	US-09-252-991A-18823
25	21	72.4	552	US-02-385-028-3
26	21	72.4	552	US-09-726-614-3
27	21	72.4	552	US-09-385-040-3

; ORGANISM: *Buccalyptus grandis*
US-09-640-211A-775

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Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 PXXXXLTXXP 10
Db 140 PSSSLTESP 149

RESULT 3

US-09-2152-991A-26404

Sequence 2, Application US/09252991A
; Patent No. 6551755

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196-136 CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18 PRIORITY APPLICATION NUMBER: -US 60/074,788

PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190

PRIORITY FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 26404 LENGTH: 221

TYPE: PRT ; ORGANISM: *Pseudomonas aeruginosa*

US-09-252-991A-26404

Query Match 75.9%; Score 22; DB 4; Length 221;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;Qy 1 PXXXXLTXXP 10
Db 64 PLASTLSSP 73RESULT 4
US-09-640-211A-920Sequence 920, Application US/09640211A
; GENERAL INFORMATION:

APPLICANT: Wood, Marion A.

APPLICANT: Shenk, Michael A.

APPLICANT: McGrath, Annette

TITLE OF INVENTION: Compositions and Methods for the

TITLE OF INVENTION: Modification of Gene Transcription

FILE REFERENCE: 11000-1021CJU CURRENT APPLICATION NUMBER: US/09/640,211A

CURRENT FILING DATE: 2000-08-16 NUMBER OF SEQ ID NOS: 2368

SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 920 LENGTH: 286

TYPE: PRT ; ORGANISM: *Eucalyptus grandis*

US-09-640-211A-920

Query Match 75.9%; Score 22; DB 4; Length 286;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;Qy 1 PXXXXLTXXP 10
Db 273 PSSSLTESP 282

RESULT 5
US-09-460-617-2
; Sequence 2, Application US/08460617

; Patent No. 5914114

GENERAL INFORMATION:

APPLICANT: Casrels, Frederick J

TITLE OF INVENTION: Method of Raising Antibodies Against E. coli

NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:

ADDRESSEE: Hendricks and Associates

STREET: 9669 A Main Street CITY: Fairfax STATE: VA COUNTRY: US ZIP: 22031

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/460,617 FILING DATE: 02-JUN-1995

CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION:

NAME: Hendricks, Glenna REGISTRATION NUMBER: 32,535 REFERENCE/DOCKET NUMBER: cas460

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-425-4250 TELEFAX: 703-425-2767

INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids TYPE: amino acid STRANDEDNESS: single

TOPOLogy: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:

ORGANISM: *E. coli*

US-08-460-617-2

RESULT 6
PCT-US95-08730-1

Sequence 1, Application PC/TUS9508730

GENERAL INFORMATION:

APPLICANT: Cassels, Frederick

APPLICANT: Anderson, Jeffrey

APPLICANT: Carter, John Mark

TITLE OF INVENTION: Methods of Raising Antibodies Against E. coli of the Family CSF-CFA./1

TITLE OF INVENTION: Methods of Raising Antibodies Against E. coli of the Family CSF-CFA./1 NUMBER OF SEQUENCES: 15 CORRESPONDENCE ADDRESS:

ADDRESSEE: Glenna Hendricks

STREET: P.O. Box 2509

CITY: Fairfax

STATE: VA

COUNTRY: USA ZIP: 22031

RESULT 2

Q7ZGR4 PRELIMINARY; PRT; 799 AA.
 ID 07ZGR4; PRELIMINARY; PRT; 799 AA.
 AC DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DB Envelope glycoprotein (Fragment).
 Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 MEDLINE=2234755; PubMed=12459786; DOI=10.1038/nature01200;
 RA Allen T.M., Altfeld M., Yu X.G., Johnston M.N., Agrawal D.,
 RA Korber B.T., Montefiori D.C., O'Connor D.H., Davis B.T., Lee P.K.,
 RA Mairer E.L., Harlow J., Goulder P.J.R., Brander C., Rosenberg E.S.,
 RA Walker B.D.;
 RT "HIV-1 superinfection despite broad CD8+ T-cell responses containing
 RT replication of the primary virus.";
 RL Nature 420:434-439(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Allain T.M., Altfeld M., Yu X.G., Johnston M.N., Agrawal D.,
 RA Korber B.T., Montefiori D.C., O'Connor D.H., Davis B.T., Lee P.K.,
 RA Mairer E.L., Harlow J., Goulder P.J.R., Brander C., Rosenberg E.S.,
 RA Walker B.D.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY247251; AAP12634.1; -.
 DR HSSP; P05877; INJ0.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0055198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR Pfam; PF00515; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KW Transmembrane.
 FT NON_TER
 SQ 799 AA; 799 MW; 655B25158831460A CRC64;

Query Match Similarity 79.3%; Score 23; DB 2; Length 799;
 Best Local Similarity 40.0%; Pred. No. 5.7e-02;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 PXXXXTXXP 10
 Db 425 PAATLTTP 434

RESULT 3

Q6PFZ6 PRELIMINARY; PRT; 942 AA.
 AC DT 29-MAR-2004 (Rel. 43, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DB Treacle protein (Treacher Collins syndrome protein homolog).
 GN Name=Tcof1;
 OS Mus musculus (Mouse).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Butheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RESULT 4

TCOF_MOUSE STANDARD; PRT; 1320 AA.
 ID TCOF MOUSE STANDARD; PRT; 1320 AA.
 AC 008784; 008857;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 05-JUL-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DB Treacle protein (Treacher Collins syndrome protein homolog).
 GN Name=Tcof1;
 OS Mus musculus (Mouse).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Butheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP TISSUE=Liver;
 RX MEDLINE=7445113; PubMed=9299440; DOI=10.1006/bbrc.1997.7229;
 RA Paznokas W.A., Zhang N., Grabley T., Jabs E.W.;
 RT "Mouse Tcof1 is expressed widely, has motifs conserved in nucleolar
 phosphoproteins, and maps to chromosome 18.";
 RL Biochem. Biophys. Res. Commun. 238:1-6(1997).
 RN [2]
 RP SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE.
 RX MEDLINE=9730169; PubMed=9158147; DOI=0.1093/hmg/6.5.727;
 RA Dixon J., Hovanes K., Shiang R., Dixon M.J.;
 RT "Sequence analysis, identification of evolutionary conserved motifs
 and expression analysis of murine tcof1 provide further evidence for a
 potential function for the gene and its human homologue, Tcof1.";
 RL Hum. Mol. Genet. 6:727-737(1997).
 RN [3]
 RP SEQUENCE OF 1-1314 FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;

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Om protein - protein search, using sw model

Run on: October 26, 2005, 04:37:41 ; Search time 39 Seconds
 (without alignments)
 24.671 Million cell updates/sec

Title: US-10-088-724c-63
 Perfect score: 29
 Sequence: 1 PXXXXLTXXP 10

Scoring table: BloSUM62
 Gapop 10.0 , Gapext: 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score % Query Match Length DB ID Description

Result No.	Score	%	Query	Match	Length	DB	ID	Description
1	23	79.3	JC5630	1320	2	JC5630		TCOF1 protein - mouse
2	22	75.9	T5215	462	2	T5215		myrosinase-binding
3	22	75.9	B95560	462	2	B95560		probable mucin-like
4	22	75.9	T43481	589	2	T43481		phospholamban-TRNA
5	22	75.9	T38232	589	2	T38232		GTPase-activating
6	22	75.9	A56033	847	2	A56033		hypothetical protein
7	21	72.4	D72466	111	2	D72466		hypothetical protein
8	21	72.4	T33597	262	2	T33597		hypothetical protein
9	21	72.4	T49323	276	2	T49323		Dreg-5 protein - f
10	21	72.4	S62241	298	2	S62241		hypothetical protein
11	21	72.4	T20336	432	2	T20336		two-component sens
12	21	72.4	A11674	459	2	A11674		hypothetical protein
13	21	72.4	T16295	484	2	T16295		hypothetical protein
14	21	72.4	D9651	501	2	D9651		cerebroside-sulfat
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17	21	72.4	M6403	546	2	M6403		phosphoglucomutase
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19	21	72.4	G9018	546	2	G9018		phosphoglucomutase
20	21	72.4	E70550	547	2	E70550		teracycline resis
21	21	72.4	B40046	578	2	B40046		phaseolin G-box bi
22	21	72.4	T10862	614	2	T10862		phaseolin G-box pro
23	21	72.4	T20981	637	2	T20981		phaseolin G-box bi
24	21	72.4	T10861	642	2	T10861		hypothetical prote
25	21	72.4	T00334	925	2	T00334		Lola-like protein
26	21	72.4	T13167	1010	2	T13167		CBP protein - hum
27	21	72.4	JC5795	1045	2	JC5795		probable chitin gly
28	21	72.4	T42022	1103	2	T42022		plasmid replicatio
29	21	72.4	T08322	1128	1	T08322		

ALIGNMENTS

RESULT 1

JC5630
 TCOF1 protein - mouse
 C;Species: Mus musculus (house mouse)

C;Date: 14-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004

C;Accession: JC5630
 R;Paznekas, W.A.; Zhang, N.; Gridley, T.; Jabs, E.W.
 Biochem. Biophys. Res. Commun. 238, 1-6, 1997

A;Title: Mouse-TCOF1-is-expressed-wide, has motif conserved in nucleolar phosphoprotein

A;Reference number: JC5630; MVID:97445113; PMID:9299440

A;Accession: JC5630
 A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-1320 <PAZ>

A;Cross-references: UNIPROT:008784; DBPI:AF001794; NID:92109458; PID:AB71347.1; PID:921

A;Comment: This protein is a nucleolar phosphoprotein with 82 potential phosphorylation sites.

Query Match Best Local Similarity 79.3%; Score 23; DB 2; Length 1320;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	1 PXXXXLTXXP 10	Db	425 PAATLTISP 434

RESULT 2

T5215
 myrosinase-binding protein [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004

C;Accession: T5215
 R;Benedetti, C.B.; Turcinelli, S.R.; Capella, A.N.; Arruda, P.

submitted to the EMBL Data Library, March 1998

A;Description: Isolation of an Arabidopsis cDNA specifically expressed in flowers and hon

A;Reference number: Z225962

A;Accession: T5215
 A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-462 <BEN>

A;Cross-references: UNIPROT:065187; EMBL:AF054906; PIDN:AAC08601.1

Query Match Best Local Similarity 75.9%; Score 22; DB 2; Length 462;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	1 PXXXXLTXXP 10	Db	148 PISSLITPP 157

nitrite reductase
 proliferation pote
 GT1 protein - mouse
 probable polyketid
 hypothetical prote
 T-cell receptor be
 hypothetical prote
 hypothetical prote
 hypothetical prote
 fimbrial protein c
 hypothetical prote
 bcl-2-associated p
 conserved hypothet
 hypothetical prote
 cytidylate kinase
 US4 protein - huma

RESULT 3	R;Biological Process: hyposmotic stress response -> biological process	B96560	Query Match Score: 75.9%; Score: 22; DB: 2; Length: 580; Best Local Similarity: 40.0%; Pred. No.: 1.1e+02; Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;	Db	1 PXXXXLTXXP 10
RESULT 4	R;Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huijzer, L.	T96560	Query Match Score: 75.9%; Score: 22; DB: 2; Length: 580; Best Local Similarity: 40.0%; Pred. No.: 1.1e+02; Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;	Db	20 PSTATSLRTP 29
RESULT 5	R;Authors: Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Hunter, J.L.; Jenkins, J.; Johnson-Hobson, C.; Khan, S.; Khaykin, E.; Kim, C.C.; Li, J.; Lin, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luhrs, J.S.; Maiti, R.; Marzali, A.; Rizzoli, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.	T38232	Query Match Score: 75.9%; Score: 22; DB: 2; Length: 580; Best Local Similarity: 40.0%; Pred. No.: 1.1e+02; Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;	Db	1 PXXXXLTXXP 10
RESULT 6	R;Authors: Koehler, K.; Bever, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.	A56039	Query Match Score: 75.9%; Score: 22; DB: 2; Length: 580; Best Local Similarity: 40.0%; Pred. No.: 1.1e+02; Matches: 4; Conservative: 0; Mismatches: 6; Indels: 0; Gaps: 0;	Db	90 RSTTSLTISP 99
RESULT 7	R;Authors: Maekawa, M.; Li, S.; Iwanatsu, A.; Morishita, T.; Yokota, K.; Imai, Y.; Kohsaka, S.; Nakai, M.; Cell, Biol, 14, 6879-6885, 1994	D72466	Query Match Score: 75.9%; Score: 22; DB: 2; Length: 847; Best Local Similarity: 40.0%; Pred. No.: 1.7e+02; Matches: 4; Conservative: 0; Mismatches: 6; Indels: 0; Gaps: 0;	Db	6 PAAALTEAP 15